We claim:

1. A method for creating a peptide and/or protein database comprising the steps of:

generating a 2-D separation of peptides and/or proteins of a first source;

generating a 2-D separation of peptides and/or proteins of a second source;

generating an electronic image of the 2-D separation of peptides and/or proteins of the first source;

generating an electronic image of 2-D separation of peptides and/or proteins of the second source;

warping one of the electronic images of the 2-D separation of peptides and/or proteins to the other image;

analyzing the two 2-D separation of peptides and/or proteins of the first and second sources to determine peptide and/or protein spots common to both tissues;

confirming commonality of at least a portion of the peptide and/or protein spots common in both the two 2-D separation of peptides and/or proteins;

recording in a peptide and/or protein database all peptide and/or protein spots common to both tissues as being the same in response to positive confirmation of the portion of the spots common to both 2-D separation of peptides and/or proteins;

analyzing peptide and/or protein spots not common to both 2-D separations; and

recording in the peptide and/or protein database results of said analyzing the peptide and/or protein spots not common to both 2-D separations.

2. The method for creating a peptide and/or protein database as set forth in claim 1, wherein said steps of generating the electronic images of the 2-D separation of peptides and/or proteins of the first and second sources comprises scanning the 2-D electrophoresis gels.

3. The method for creating a peptide and/or protein database as set forth in claim 2, wherein said step of warping one of the electronic images of the 2-D separation of peptides and/or proteins to the other comprises electronically stretching, rotating and/or shrinking

portions of the one of the electronic images so that at least a portion of spots on the 2-D electrophoresis gels are brought into alignment with one another.

4. The method for creating a peptide and/or protein database as set forth in claim 3, wherein said step of analyzing the two 2-D separation of peptides and/or proteins of the first and second sources to determine peptide and/or protein spots common to both tissues comprises the step of determining which peptide and/or protein spots in the two gel images are aligned with one another.

5. The method for creating a peptide and/or protein database as set forth in claim 4, wherein said step of confirming commonality between at least a portion of the peptide and/or protein spots common in both the two 2-D separation of peptides and/or proteins comprises the steps of:

excising several of the aligned spots common to both 2-D electrophoresis gels from the gels; and

subjecting the excised spots to mass spectrometry analysis.

6. The method for creating a peptide and/or protein database as set forth in claim 5, wherein said step of analyzing peptide and/or protein spots not common to both 2-D separations comprises the steps of:

excising several of the spots not common to both 2-D electrophoresis gels from the gels; and

subjecting the excised spots to mass spectrometry analysis.

7. The method of claim 1, wherein said first source and said second source are two different tissues.

8. The method of claim 1, wherein said first source and said second source are samples obtained from two individuals of a population.

9. The method of claim 7, wherein said tissues are from one individual or from genetically identical individuals.

10. The method of claim 1, wherein said first source and said second source are two different cells.

11. The method of claim 1, wherein said first source and said second source are two different organelles.

12. A method for identifying a polypeptide in a sample from a mammal of a randomly breeding population, comprising:

(a) characterizing said polypeptide by isoelectric point;

(b) characterizing said polypeptide by molecular weight; and

(c) identifying tissues of said subject where said polypeptide is found, wherein at least 5 tissues are examined;

to yield distinguishing parameters of said polypeptide comprising isoelectric point, molecular weight and tissue distribution;

(d) comparing said distinguishing parameters of said polypeptide with distinguishing parameters of previously tested polypeptides of a set; and

(e) determining whether a previously tested polypeptide of said set has said distinguishing parameters of said polypeptide,

wherein said polypeptide is identified as being said previously tested polypeptide when said distinguishing parameters of said polypeptide match the parameters of said previously tested polypeptide, or adding said polypeptide and said distinguishing parameters to said set when said distinguishing parameters of said polypeptide are unique to said set.

13. The method of claim 12, wherein said set comprises identifying patterns of at least 10 proteins.

14. The method of claim 13, wherein said set comprises identifying patterns of at least 20 proteins.

15. The method of claim 14, wherein said set comprises identifying patters of at least 30 proteins.

16. The method of claim 15, wherein said set comprises identifying patterns of at least 40 proteins.

17. The method of claim 16, wherein said set comprises identifying patterns of at least 50 proteins.

18. The method of claim 12, further comprising characterizing said polypeptide to yield one or more additional distinguishing parameters of said polypeptide.

19. The method of claim 18, wherein said additional distinguishing parameter comprises a partial primary amino acid sequence of said polypeptide, or fragment thereof.

20. The method of claim 18, wherein said additional distinguishing parameter is mass spectrometry data of said polypeptide, or fragment thereof.

21. The method of claim 12, wherein at least 7 tissues are examined.

22. The method of claim 21, wherein at least 9 tissues are examined.

23. The method of claim 22, wherein at least 11 tissues are examined.

24. The method of claim 23, wherein at least 13 tissues are examined.

25. The method of claim 12, where said step (d) is conducted by a data processing means.

26. The method of claim 12, wherein said steps (a) and (b) are obtained by two-dimensional gel electrophoresis.

27. The method of claim 20, wherein said spectrometry data is obtained by matrix-assisted laser desorption ionization (MALDI).

28. The method of claim 27, wherein said MALDI spectrometry comprises time of flight (TOF) analysis.

29. The method of claim 25, further comprising characterizing the spatial relationship of said polypeptide with one or more of said previously tested polypeptides on stained two dimensional electrophoresis gels.

30. An ordered set of elements comprising at least N elements, wherein each of said N elements is a polypeptide or a protein, wherein presence or absence of each of said N elements is determined in at least 5 tissues from a single subject; each of said elements is analyzed by mass spectrometry and N is at least 10.

31. The set of claim 30, wherein said set comprises at least 20 elements.

32. The set of claim 30, wherein said polypeptide is of unknown function.

33. The set of claim 30, wherein expression of said elements is tested in at least 7 tissues.

34. The set of claim 30, wherein an element is characterized further by having a molecular weight value.

35. The set of claim 30, wherein an element is characterized further by having an isoelectric point.

36. The set of claim 30, wherein said subject is a human.

37. The set of claim 30, wherein an element is characterized further by a cell of origin.

38. The set of claim 30, wherein an element is characterized further by an organelle of origin.

39. The set of claim 30, wherein said ordered set of elements is contained in a machine-readable storage medium.

40. A machine readable storage medium comprising digitized data of an ordered array of N elements, wherein said N elements are proteins; and wherein said digitized data comprises expression of each of said N elements in at least 5 tissues of a single subject and a mass spectrometry scan of each of said elements; and N is at least 10.

41. The medium of claim 40, comprising expression in at least 7 tissues.

42. The medium of claim 41, comprising expression in at least 9 tissues.

43. The medium of claim 42, comprising expression in at least 11 tissues.

44. The medium of claim 40, wherein N is at least 20.

45. The medium of claim 44, wherein N is at least 30.

46. The medium of claim 45, wherein N is at least 40.

47. The medium of claim 46, wherein N is at least 50.

48. A data processing system for determining identity of an element (N+1) to N elements of a database contained in a storage medium comprising:

(a) computer processing means for processing data;

(b) data storage means for storing data in said database contained in said storage medium; and

(c) means for processing data regarding comparing a parameter of said (N+1) element with said parameter of said N elements of said database,

wherein said element is a protein or polypeptide; wherein step (c) is repeated at least M times, wherein each of M parameters is examined at each iteration, wherein M is 3 or more; and wherein when said (N+1) element does not have M identical parameters of one of said N elements, said data storage means (b) adds data of said (N+1) element and of said M parameters thereof to said database to produce a new database comprising (N+1) elements.

49. The system of claim 48, wherein said element is a protein or polypeptide.

50. The system of claim 49, wherein said two of said three parameters are molecular weight and isoelectric point.

51. The system of claim 49, wherein one of said three elements is a mass spectrometry analysis of said element.

52. A method for determining whether a protein spot on a first two dimensional gel (2DG) is the same or different from a spot on a second 2DG, when protein containing samples for said first and second gel are from different sources, comprising;

establishing location of at least 10 landmark spots on each of said first 2DG and said second 2DG,

obtaining an image of said first 2DG and said second 2DG,

aligning said landmark image positions so that said landmark image positions of said second 2DG are in register with corresponding landmark image positions of said first 2DG; and

identifying a provisional identical spot image on said second 2DG that about aligns with said image of said protein spot on said first 2DG;

wherein said protein of said provisional identical spot image on said second 2DC is identified as the same protein of said protein spot of said first 2DG.

53. The method of claim 52, wherein said proteins of said landmark spots are known proteins.

54. The method of claim 52, further comprising:

subjecting a sample of said protein spot on said first 2DG and a sample of said provisional identical spot on said second 2DG to a characterizing step to yield identifying data of said proteins of said samples of said first 2DG and said second 2DG.

55. The method of claim 54, wherein said characterizing step is mass spectrometry.

56. The method of claim 54 wherein said characterizing step is determining the amino acid sequence of said protein or fraction thereof of said protein spot and said provisional identical spot.

57. The method of claim 54 further comprising:

identifying said protein spot of said first 2DG and said second 2DG as a landmark spot when said identifying data of said protein of said protein spot and said provisional identical spot are the same.

58. Hierarchical dissection or separation method comprising the steps of:

acquiring whole tissue samples from a statistically significant number of identified individuals;

analyzing the whole tissues by high resolution two-dimensional electrophoresis,:

acquiring images of the resulting gels;

processing said images by superimposing landmarks of said images, wherein same images are manipulated so that all landmarks are in register;

comparing the superimposed patterns to detect differences and similarities; and

recording said differences and similarities in a database.

59. The method of claim 58, wherein said tissue samples are separated in two or more different cell types before said analyzing step.

60. The method of claim 58, wherein said tissue samples are exposed to a cell fractionation procedure prior to said analyzing step.

61. The method of claim 59, wherein said separated cells are exposed to a cell fractionation procedure prior to said analyzing step.

62. The method claims 60, wherein said cell fractionation procedure employs multiple-parallel gradients.

63. A method of detecting proteins that have correlated expression, comprising:

comparing images of two-dimensional gels of a tissue sample from genetically similar or genetically identical individuals to detect two or more proteins with coordinated expression.

64. The method of claim 63, wherein said correlation is positive.

65. The method of claim 63, wherein said correlation is negative.

66. A method of removing proteins from a tissue sample prior to a method for separating the remaining proteins in said sample comprising; exposing said tissue sample to a solid matrix comprising a plurality of antibodies, wherein each of said antibodies specifically binds to a tissue protein, wherein said antibodies bind to at least five tissue proteins; removing said tissue sample from said solid matrix; and separating said remaining tissue proteins.

67. The method of claim 66, wherein said solid matrix is a bead.

68. The method of claim 66, wherein said separating step is isoelectric focusing.

69. The method of claim 66, wherein said five proteins comprise albumin.

70. The method of claim 69, wherein said five proteins comprise immunoglobulin.

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